

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
- (ii) TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 - (B) STREET: 3330 HILLVIEW AVENUE
 - (C) CITY: PALO ALTO
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33954
 - (C) REFERENCE/DOCKET NUMBER: PF-0027US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-855-0572

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: 223187
 - (B) CLONE: HUMAN PANCREAS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG	60
GGGCTCACTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG	120
ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA	180
GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG	240
GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGC	289

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUMAN PANCREAS
- (B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Trp	Leu	Leu	Leu	Ile	Ala	Ala	Ala	
1				5				10						15		
Phe	Ser	Pro	Gln	Gly	Leu	Thr	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	
			20				25						30			
Cys	Phe	Asn	Leu	Ala	Asn	Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	
		35					40					45				
Tyr	Arg	Arg	Ile	Thr	Ser	Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	
	50					55					60					
Lys	Thr	Lys	Leu	Ala	Lys	Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp	
	65				70					75					80	
Val	Gln	Asp	Ser	Met	Lys	Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	
				85				90						95		
Pro																

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUMAN PANCREAS

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG      60
ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTCCTCA AGTACAGCCA AAGGAAGATT      120
CCCGCCAAGG TTGTCCGCAG CTACCGGAAG CAGGAACCAA GCTTAGGCTG CTCCATCCCA      180
GCTATCTGT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTGCAGA CCCAAAGGAG      240
CTCTGGGTGC AGCAGCTGAT GCAGCATCTG GACAAGACAC CATCCCCACA GAAACCAGCC      300
CAGGGCTGCA GGAAGGACAG GGGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA      360
GGCTGCAAGA GGAAGGACAG GTCACAGACC CCTAAAGGGC CA                          402
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUMAN PANCREAS

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
1              5              10              15
Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
20              25              30
Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
35              40              45
Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
50              55              60
Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
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65

70

75

80

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
85 90 95

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
100 105 110

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
115 120 125

Gln Thr Pro Lys Gly Pro
130